FOR THE RECORD

Zhaoshu Zeng,[1] *Ph.D; Xudong Zheng,*[1] *Ph.D.; Guangzheng Zhang,*[1] *M.D.; Yunliang Zhu,*[1] *Ph.D.; Xiansheng Meng,*[2] *M.D.; Zhide Xiang,*[2] *M.D.; Baolong Yuan,*[2] *M.D.; Chunling Wu,*[2] *M.D.; and Ziming Dong,*[1] *M.D., Ph.D.*

Genetic Data of Six STR Loci of Han Population in Henan Province (Central China)

POPULATION: Chinese.

KEYWORDS: forensic science, DNA typing, short tandem repeats, polymerase chain reaction, U.C. Han in U.C. Henan, China, population genetics, U.C. China, CSF1PO, TH01, TPOX, D2S1338, D16S539, D19S433

Blood samples were collected from unrelated individuals of Chinese Han ethnic group in Zhengzhou of Henan. DNA was extracted using Chelex method (1). Target DNA of 0.5–2 ng was amplified using GeneAmp PCR System 9700 (Applied Biosystems, Foster City, CA) following the protocols described in the AmpFLSTR Identifiler[TM] PCR amplification kits (PE Applied Biosystems) with the exception that the PCR volume was 25 µl. DNA typing was carried out with the ABI 3100 Genetic Analyzer (Applied Biosystems) within which PCR products were separated, and GeneScan analysis software (version 3.1.2) was used to analyze the results. Genotypes were determined by comparison with allelic ladder using Genotyper DNA fragment analysis software (version 2.5) (Applied Biosystems). Alleles were designated following the DNA recommendations of the DNA commission of the ISFH (2). Statistical parameters like power of discrimination, polymorphic information content, power of exclusion, paternity index, matching probability, and heterozygosity observed were calculated using PowerStats V12 (3–5). Test for Hardy–Weinberg equilibrium was carried out according to Hou's method (6). No deviation from Hardy–Weinberg equilibrium was observed.

The complete data can be accessed at dnadata-zeng@sohu.com.

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Additional information and reprint requests:
Zhaoshu Zeng, Ph.D.
Department of Forensic Medicine
Medical School of Zhengzhou University
Zhengzhou, Henan 450052
China
E-mail: zs_zeng@yahoo.com

[1]Department of Forensic Medicine, Medical School of Zhengzhou University, Zhengzhou, Henan 450052, China.
[2]Department of Forensic Medicine, Police Station of Zhengzhou, Zhengzhou, Henan 450004, China.
This work was never been presented or posted before.

TABLE 1—*Allele frequencies and statistics of 6 STRs in Henan population.*

Allele	CSF1PO	TH01	TPOX	D2S1338	D16S539	D19S433
6		0.087				
7	0.002	0.252				
8		0.07	0.565		0.007	
9	0.036	0.529	0.108		0.313	
9.3		0.036				
10	0.233	0.026	0.019		0.149	
11	0.231		0.279		0.216	0.002
12	0.392		0.029		0.214	0.058
12.2						0.012
13	0.091				0.089	0.286
13.2						0.036
14	0.014				0.012	0.236
14.2						0.113
15						0.075
15.2						0.135
16				0.012		0.014
16.2						0.031
17				0.077		
17.2						0.002
18				0.115		
19				0.161		
20				0.111		
21				0.019		
22				0.05		
23				0.243		
24				0.125		
25				0.072		
26				0.007		
27				0.007		
PIC	0.68	0.60	0.53	0.84	0.75	0.80
PD	0.883	0.814	0.782	0.960	0.914	0.940
PE	0.470	0.367	0.275	0.735	0.569	0.678
HE	0.726	0.659	0.587	0.870	0.784	0.841
P	0.876	0.655	0.881	0.724	0.935	0.471

PIC, polymorphic information content; PD, power of discrimination; PE, power of exclusion; HE, observed heterozygosity; P, Hardy–Weinberg disequilibrium, exact test.